-12014

-6038  -5155  -3387  -2394  -594  +33

1

5976  6659  8627  9620  11420 12047
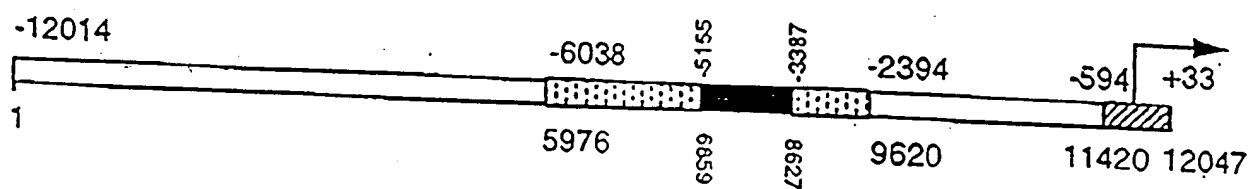
FIGURE 1

```
HKLK2.LA0    (6998)   AA-CTGAGCCTTGATTATATTG-GAGCTTGGTTGCA-CAG-ACATGTCGA
                      :: :: :: : ::: :::: :: : :::      :   ::: ::: :: :
PSE          ( 509)   AATCT-AG-C-TGA-TATAGTGTG-GCTCAAAACCTTCAGCACAAATC-A

HKLK2.LA0    (7044)   CCACCTTCATGGCTGAACTTTAGTACTTAGCCCCTCCAGACGTCTACAGC
                       :::: : : :: : : :: : : :: :: : : ::: :: :: :::
PSE          ( 553)   -CACCGTTA-GACT--A-TCTGGT--GT-G--GC-CCAAAC--CTTCAGG

HKLK2.LA0    (7094)   TGATAGGCTGTAACCCAACAT-TGTCACCATAAATCACATTGTTAGACTA
                      ::: :     :   :: : :: :: :: ::   :: : ::: ::   :: :
PSE          ( 590)   TGA-ACAAAGGGACTCTA-ATCTGGCAGGAT-ATTC-CA----AAG-C-A

HKLK2.LA0    (7143)   TCCAGTG-TGGCC-CAAGCTCCCGTGTAAACACAGGCACTCTAAACAG--
                      :  :: : :::   : :    :     ::: : : :     ::: ::
PSE          ( 630)   T-TAGAGATGACCTCTTGC-AAAG-AAAAAGAAATGGAAAAGAAAAAGAA

HKLK2.LA0    (7189)   -G-CAGGATATTTCAAAAGCTT-AGAGATGACCTCCCAGGAGCTGAATGC
                       :  :::: :  :    ::::  :::::::::::: :::: :::: :
PSE          ( 677)   AGAAAGGAAAAAAAAAAAAAAAAGAGATGACCTCTCAGGCTCTGAGGGG

HKLK2.LA0    (7236)   AAA-GACCTGGCCTCTTTGGGCAAGGAGAATCCTTTACCGCACACTCTCC
                      ::: : ::::    :::::: :::::: : :::      ::::: :::::
PSE          ( 727)   AAACG-CCTGAGGTCTTTGAGCAAGGTCAGTCCTCTGTTGCACAGTCTCC

HKLK2.LA0    (7285)   TTCACAGGGTTATTGTGAGGATCAAATGTGGTCATGTGTGTGAGACACCA
                      :::::::: :::::::: ::::::::::::::::: :::: :::: :::::
PSE          ( 776)   CTCACAGGGTCATTGTGACGATCAAATGTGGTCACGTGTATGAGGCACCA
                                                                  : ---
HKLK2.LA0    (7335)   GCACATGTCTGGCTGTGGAGAGTGACTTCTA--TGTGTGCTAACATTGCT
                      :::::::: :::::: ::: ::::: : : ::: :::: :: :::
PSE          ( 826)   GCACATGCCTGGCTCTGGGGAGTGCCGTGTAAGTGTATGCTTGCACTGCT
                      :: :      :         :: :       ::: : : :    :
HKLK2.LA0    (7383)   GAGTGCTAAGAAAGTATTAGGCATGGCT-TTCAGCACTCACAGATGCTCA
                      :: :::: : : : ::: ::  : ::::::: ::::::::::::::::::
PSE          ( 876)   GAATGCTTGGGATGTGTCAGGGAT-TATCTTCAGCACTTACAGATGCTCA
                      :: :      :     :            :      :    :    ::
```

**FIGURE 2A**

```
HKLK2.LA0    (7432)   TCTAATCCTCACAACATGGCTACAGGG-TGGGCACTACTAGCCTCATTTG
                      ::  ::::::::::  :::   :::   :::::  : :::: :::::::::
PSE          ( 925)   TCTCATCCTCACAGCATCACTA-TGGGATGGGTATTACTGGCCTCATTTG
                      :  ::       : ::  :         :::     :  : ::  : :

HKLK2.LA0    (7481)   ACAGAGGAAAG-GACTGTGGATAAGAAGGGGGTGACCAATAGGTCAGAGT
                      :  ::  ::::::  :  ::::::: : :::: :: :::: :::  ::: :
PSE          ( 974)   ATGGA-GAAAGTGGCTGTGGCTCAGAAAGGGGGGGACCACTAGACCAGGGA
                      :  :  :  :               :      :            :

HKLK2.LA0    (7530)   CATTCTGGATGCAAGGGG-CTCCAGAGGACCATGATTAGACATTGTCTGC
                      ::  ::::::::::  ::::  ::::::::  :::::::::  :  ::  ::::
PSE          (1023)   CACTCTGGATGC-TGGGGACTCCAGA-GACCATGACCACTCACCAACTGC
                      :  :        :        :      :       ::  :  ::      :

HKLK2.LA0    (7579)   AGAGAAATT----ATGG-CTGGATGTCTCTGCCCCGGAAAGGG-GGA--T
                      :::::::::   ::: :: :::::::  ::: :: ::: :::: ::: :
PSE          (1071)   AGAGAAATTAATTGTGGCCT-GATGTCCCTGTCCTGGAGAGGGTGGAGGT
                      ::  :     :    :    :  :: :         :        ::   ::

HKLK2.LA0    (7621)   GCACTTTCCTTGACCCCCTATCTCAGATCTTGACTTTGAG-GTTATCTCA
                      : .::  :::  : :::  :::  :  :    :::: :: : : : :::
PSE          (1120)   GGACCTTCACTAACCTCCTACCT-TGACCCTCTCTTTTAGGGCTCTTTCT
                      :     :   :     :  :        ::  :         :  :      :

HKLK2.LA0    (7670)   GACTTCCTCTATGATACCAGGAGCCCATCATAATCTCTCTGTGTCCTCTC
                      :::  :::  :  :::  :::  ::::  :::    :::    :: ::
PSE          (1169)   GACCTCCACCATGGTACTAGGA-CCC--CATTGTAT-TCTGT-ACC-CT-
                      ::    :    :            ::   ::    :  :  : :

HKLK2.LA0    (7720)   CCCTTCCTCAGTCTTACTG-CCCACTCTTCCCAGCTCCATCTCCAGCTGG
                      :  :  :  ::  ::  ::  ::: :  :: ::::  :: ::  :::::::
PSE          (1212)   --C-T--TGACTC-TA-TGACCCCCACTGCCCA-CTGCA--TCCAGCT--
                      :  :        :          :  :           ::         :

HKLK2.LA0    (7769)   CCAGGTGTAGCCACAGTACCTAACTCT-TTGCAGAGAACTATAAATGTGT
                      ::  ::  ::  :  ::::::  : : :: :  : ::  ::     : :::
PSE          (1250)   ---GG-GT--CC-C-CT-CCTATCTCTATT-CCCAG--CTGGCCA-GTGC
                      :                   :        :   ::               ::

HKLK2.LA0    (7818)   A-TCCTACAGGGGAGAAAAAAA-AAAAG-AACTCTGAAAGAGCTGACATT
                      : : :: ::: :   :         ::  :::::::::: :::::::::::
PSE          (1287)   AGT-CT-CAGTGCCCACCTGTTTGTCAGTAACTCTGAAGGGGCTGACATT
                      :   :   :   ::  ::   ::       :                   :

HKLK2.LA0    (7865)   TTACCGACTTGCAAACACATAAGCTAACCTGCCAG--TTTTGT----GCT
                      ::::  ::::::::::::  :: :::::::::::: : ::::  ::::: :::
PSE          (1335)   TTACTGACTTGCAAACAAATAAGCTAACTTTCCAGAGTTTTGTGAATGCT
                      :  :  :  :: ::  : :::::  :        ::      :   : :  :

HKLK2.LA0    (7909)   GGTAGAACT-CATGAGACTCCTGGGTCAGAGGCAAAAGATTTTATTACCC
                      ::  ::  :: : :::::::::::::::::::::::: :  ::::: : : :
PSE          (1385)   GGCAG-AGTCCATGAGACTCCTGAGTCAGAGGCAAAGGCTTTTACTGCTC
                      :::          :::         :::
```

## FIGURE 2B

```
HKLK2.LA0    (7958)  ACAGCTAAGGAGGCAGCATGAACTTTGTGTTCACATTTGTTCACTTTGCC
                     ::::::  ::  ::  :::::::::    ::     :::::::::::::
PSE          (1434)  ACAGCTTAGCAGACAGCATGAGGTTCATGTTCACATTAGTACACCTTGCC
                      :         :  ::    :  ::  ::         ::      : :

HKLK2.LA0    (8008)  CCCC--AATTCATAT-GGGATGATCAGAGCAGTTC-AGGTGGATG--G-A
                     ::::   ::  :: :::  :::: ::::::::: ::  :::::::::::::::
PSE          (1484)  CCCCCCAAATCTTGTAGGG-TGACCAGAGCAG-TCTAGGTGGATGCTGTG
                      :        :  ::   : :    ::::    :         ::    .

HKLK2.LA0    (8051)  CA-CAGGGGTTTGTGGCAAAGGTGAGCAACCTAG-GCTTAGAAATCCTCA
                     ::  :::::::::: ::  :::::  :::::: : :  ::::  :::::::::
PSE          (1532)  CAGAAGGGGTTTGTGCCACTGGTGAGAAACCT-GAGATTAGGAATCCTCA
                      :                  ::::  :              ::        :

HKLK2.LA0    (8099)  ATCTTATAAGAAGGTACT---AGCAAACTTGTC-CAGTCTTTGTATCTGA
                     ::::::::  :   ::  ::    :::::: ::::::   :::::   :::::
PSE          (1581)  ATCTTAT-ACTGGG-ACAACTTGCAAACCTG-CTCAGCCTTTGTCTCTGA
                      : :         ::       ::         ::         ::: : :

HKLK2.LA0    (8145)  CGGAGATATTATCTTTATAAT-TGGG-TTGAAAGCAGACCTACTCTGGAG
                      : ::::::::::  ::  :: : :: ::::::  :::::::::::::::::
PSE          (1628)  TGAAGATATTATCTTCATGATCTTGGATTGAAAACAGACCTACTCTGGAG
                      :     : :       ::  ::  :              ::        :

HKLK2.LA0    (8193)  GAACATATTGTATTTATTGTCCT-GAACAGTAAACAAATCTGCTGTAAAA
                     :::::::::::::  :::::::::  : :::::::::::::::::  ::   ::
PSE          (1678)  GAACATATTGTATCGATTGTCCTTG-ACAGTAAACAAATCTGTTGT--AA
                      :     :  ::   :   :  ::  :         :   :::

HKLK2.LA0    (8242)  TAGACGTTAACTTTATTATCTAAGG-CAGTAAGCAAACCTAGATCTGAAG
                     ::::  ::: :::::::::::::  :::  :::::::::::   ::  :::::: ::
PSE          (1725)  GAGACATTATCTTTATTATCT-AGGACAGTAAGCAAGCCTGGATCTG-AG
                      :

HKLK2.LA0    (8291)  -GCGATACCATCTTGCAAGGCTATCTGCTGTACAAATATGCTTGAAAAGA
                     : :::: ::::::::::::::  :  :::::  :::::: ::  ::::::
PSE          (1773)  AGAGATATCATCTTGCAAGGATGCCTGCTTTACAAACATCCTTGAAACAA
                      :

HKLK2.LA0    (8340)  TGGTCCAGAAAAGAAAACGGTATTATTGCCTTTGCTCAGAAGACACACAG
                     :::::::::::  ::::  :::  ::  :::::::::::::::::::::::::
PSE          (1823)  CAATCCAGAAAA-AAAAAGGTGTTGCTGTCTTTGCTCAGAAGACACACAG

HKLK2.LA0    (8390)  AAACATAAGAGAACCATGGAAAATTGTCTCCCAACACTGTTCACCCAGAG
                     : ::  :  :  :::::::::::  ::::: ::  :::::::::  ::::::::
PSE          (1872)  ATACGTGACAGAACCATGGAGAATTGCCTCCCAACGCTGTTCAGCCAGAG

HKLK2.LA0    (8440)  CCTTCCACTCTTGTCTGCAGGACAGTCTTAACATCCCATCATTAG-T-GT
                     :::::::::: ::::::::::::::::::::  ::: : ::: ::::   :
PSE          (1922)  CCTTCCACCCTTGTCTGCAGGACAGTCTCAACGTTCCACCATTAAATACT
                      ::  :::                            :  ::  ::      ::
```

# FIGURE 2C

```
HKLK2.LA0    (8488)    --GTCTACCACATCTGGCTTCACCGTGCCTAACCAAGATTTCTAGGTCCA
                         :::: :::::::  ::::::   ::::::::::::::  :::::::::::
PSE          (1972)    TCTTCTATCACATCCTGCTTCTTTATGCCTAACCAAG-GTTCTAGGTCCC
                         :         ::     : :   :         : :   :: : ::   :

HKLK2.LA0    (8536)    GTTCCCCACCATGTTTGGCAGTGCCCCACTGCCAACCCCAGAATAAGGGA
                        : :   : ::    ::: ::::::  : :::::::::::::::::::::: :
PSE          (2021)    GAT--CGACTGTGTCTGGCAGCACTCCACTGCCAAACCCAGAATAAGGCA
                         ::    :    ::  :    :          ::                :

HKLK2.LA0    (8586)    GTGCTCAGAATTCCGA
                        : :::::::  : ::::
PSE          (2069)    GCGCTCAGGATCCCGA
                        :         : :
```
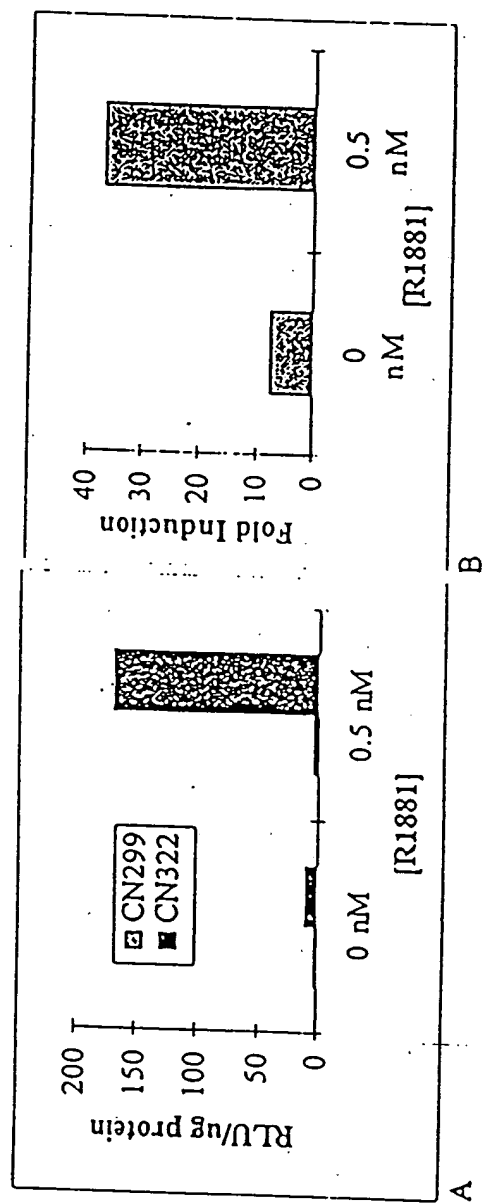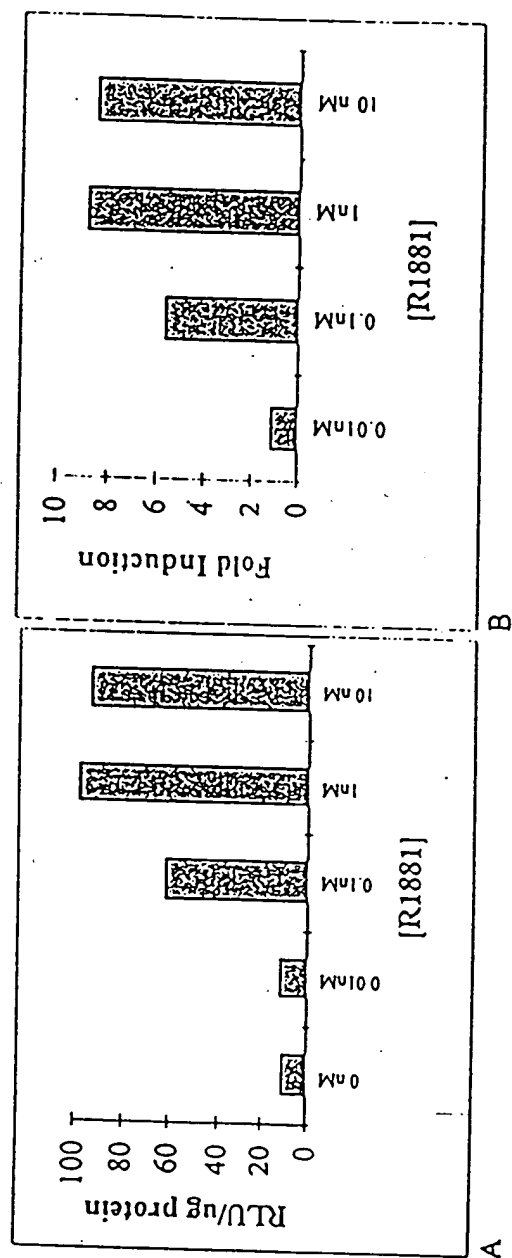
**FIGURE 2D**
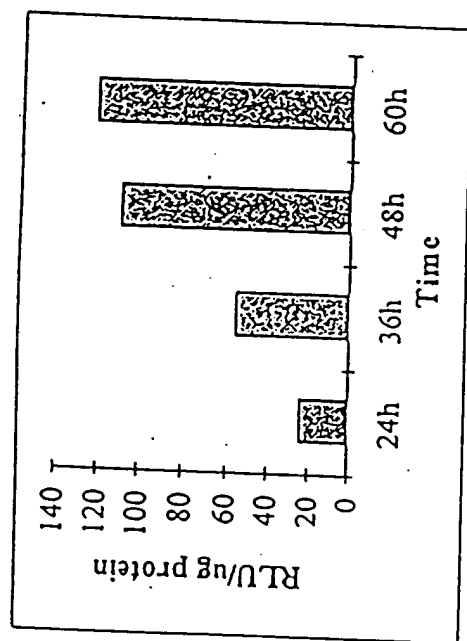
FIGURE 3

**FIGURE 4**

FIGURE 5

FIGURE 6

**FIGURE 7**
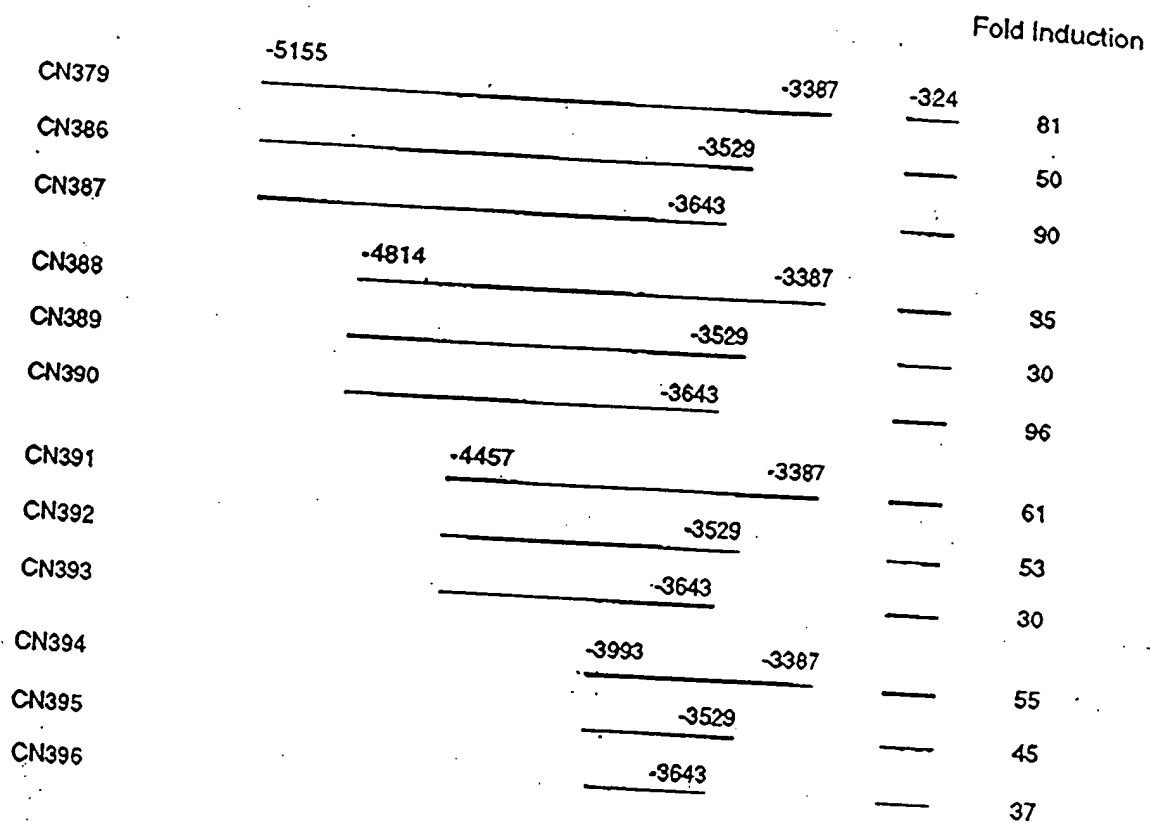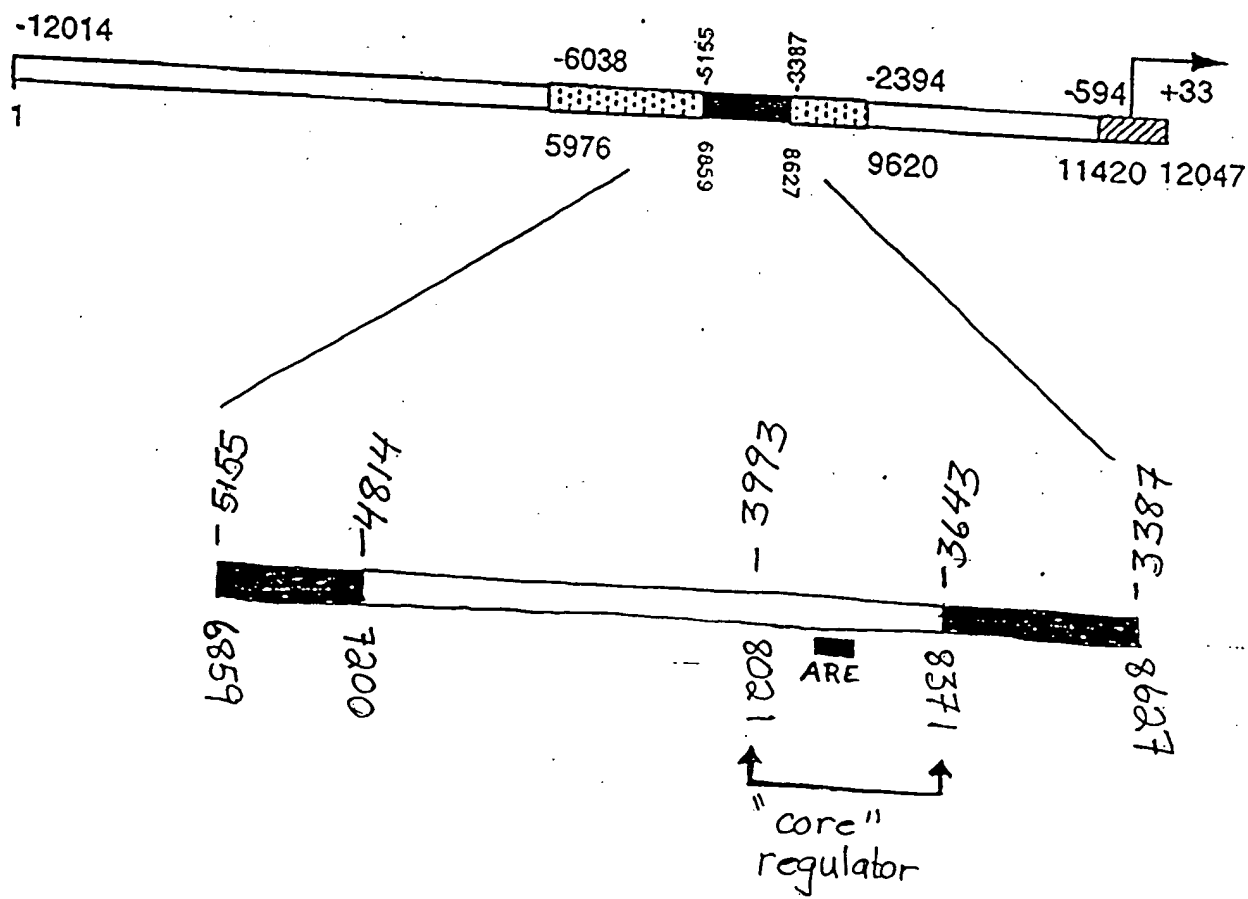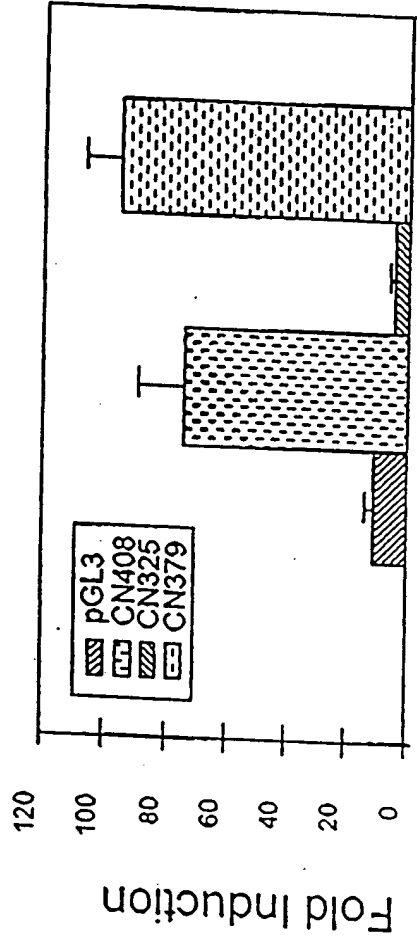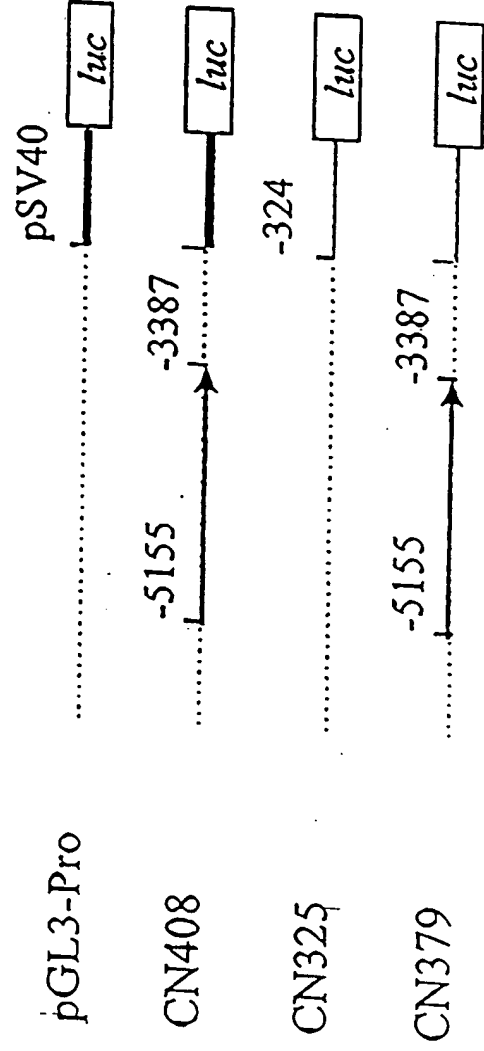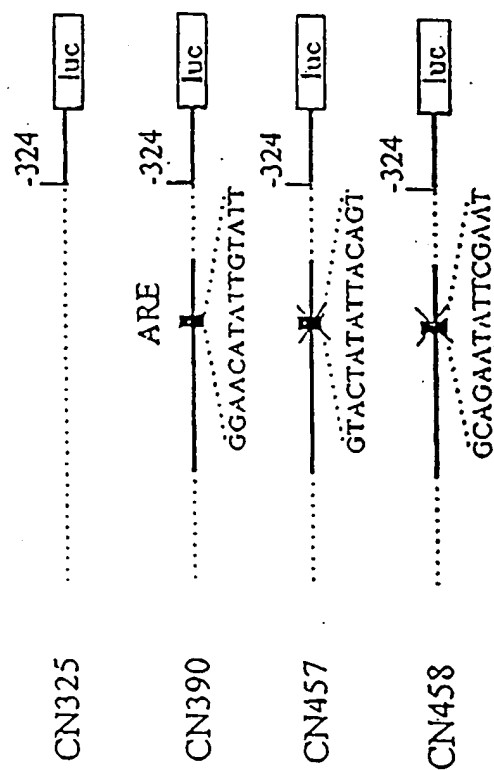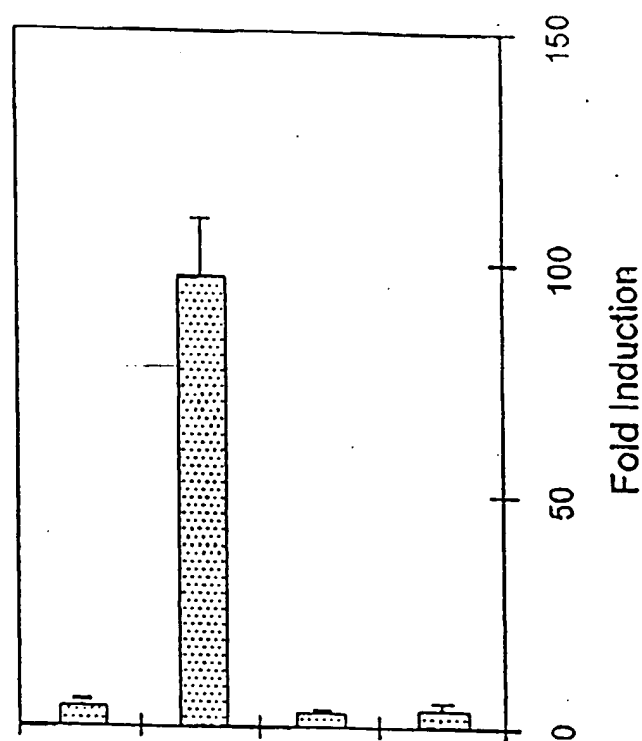
FIGURE 8

**FIGURE 9**
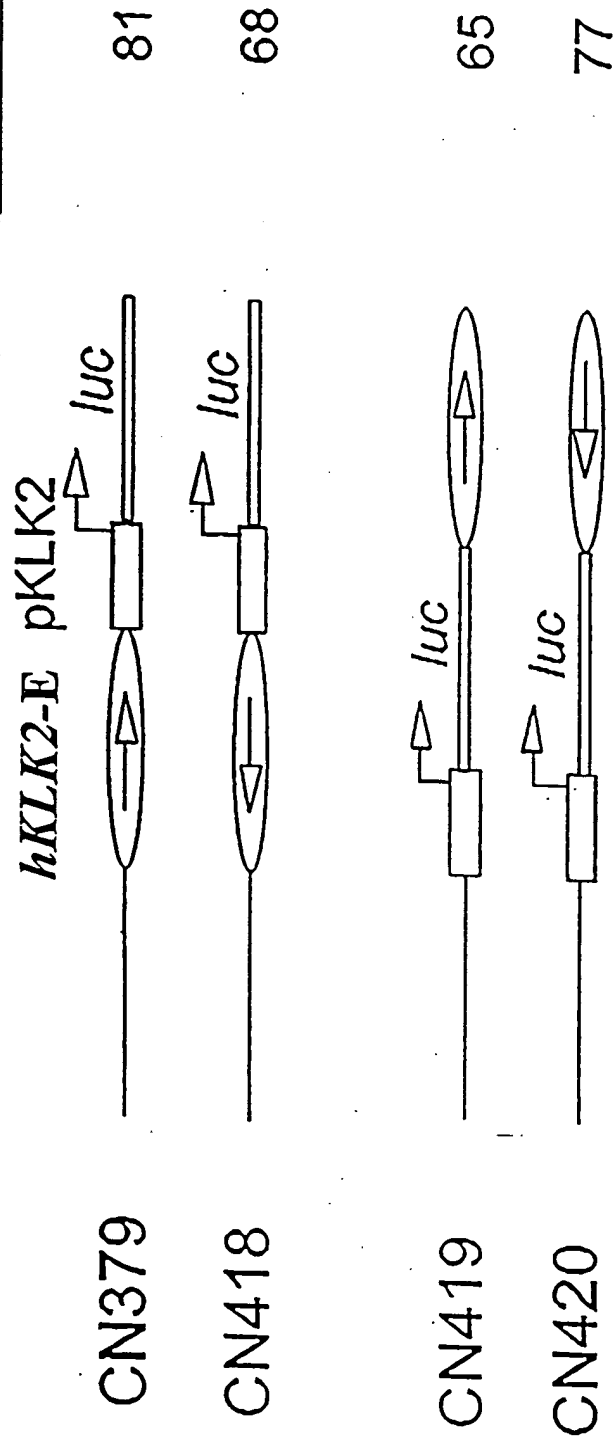
FIGURE 10
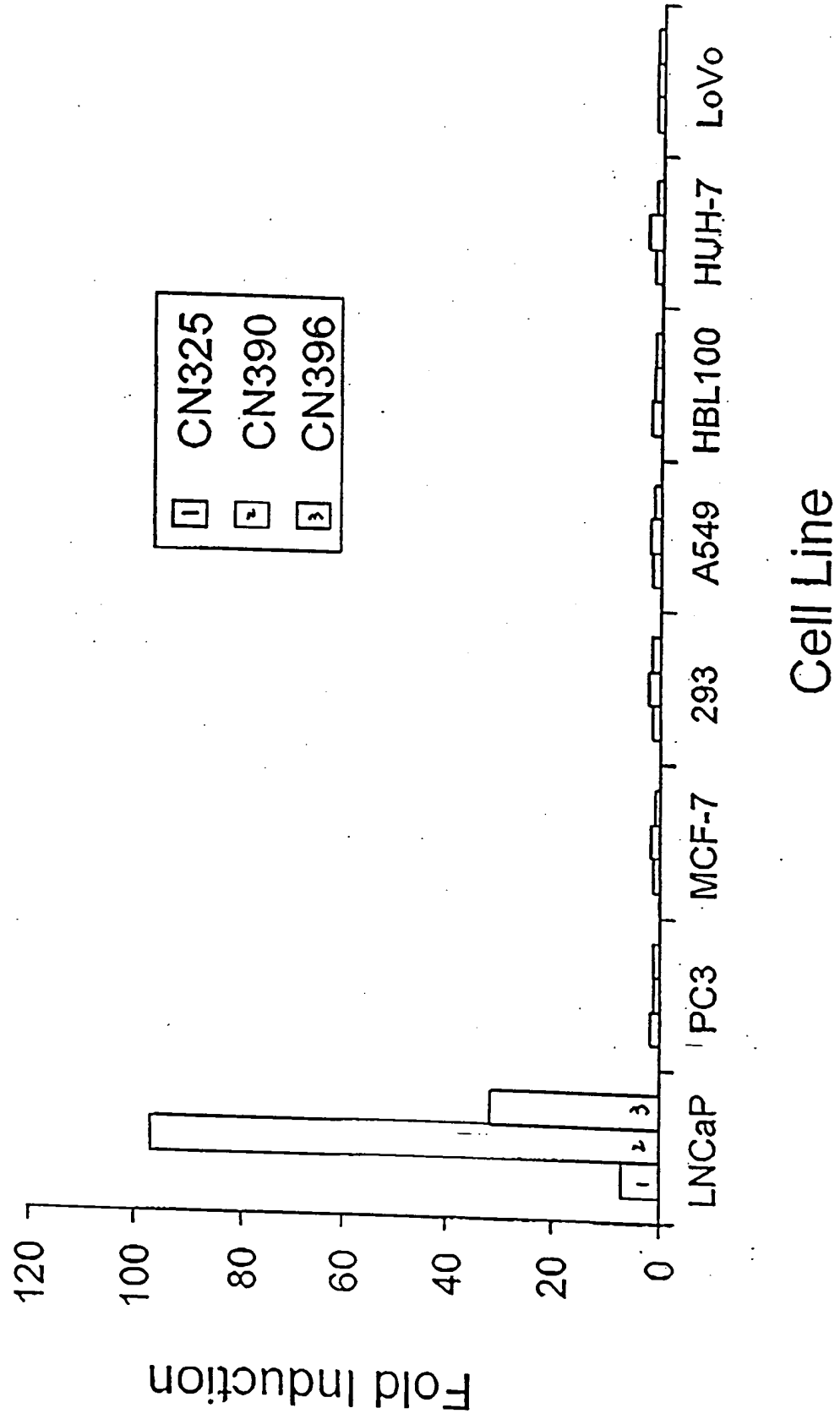
FIGURE 11
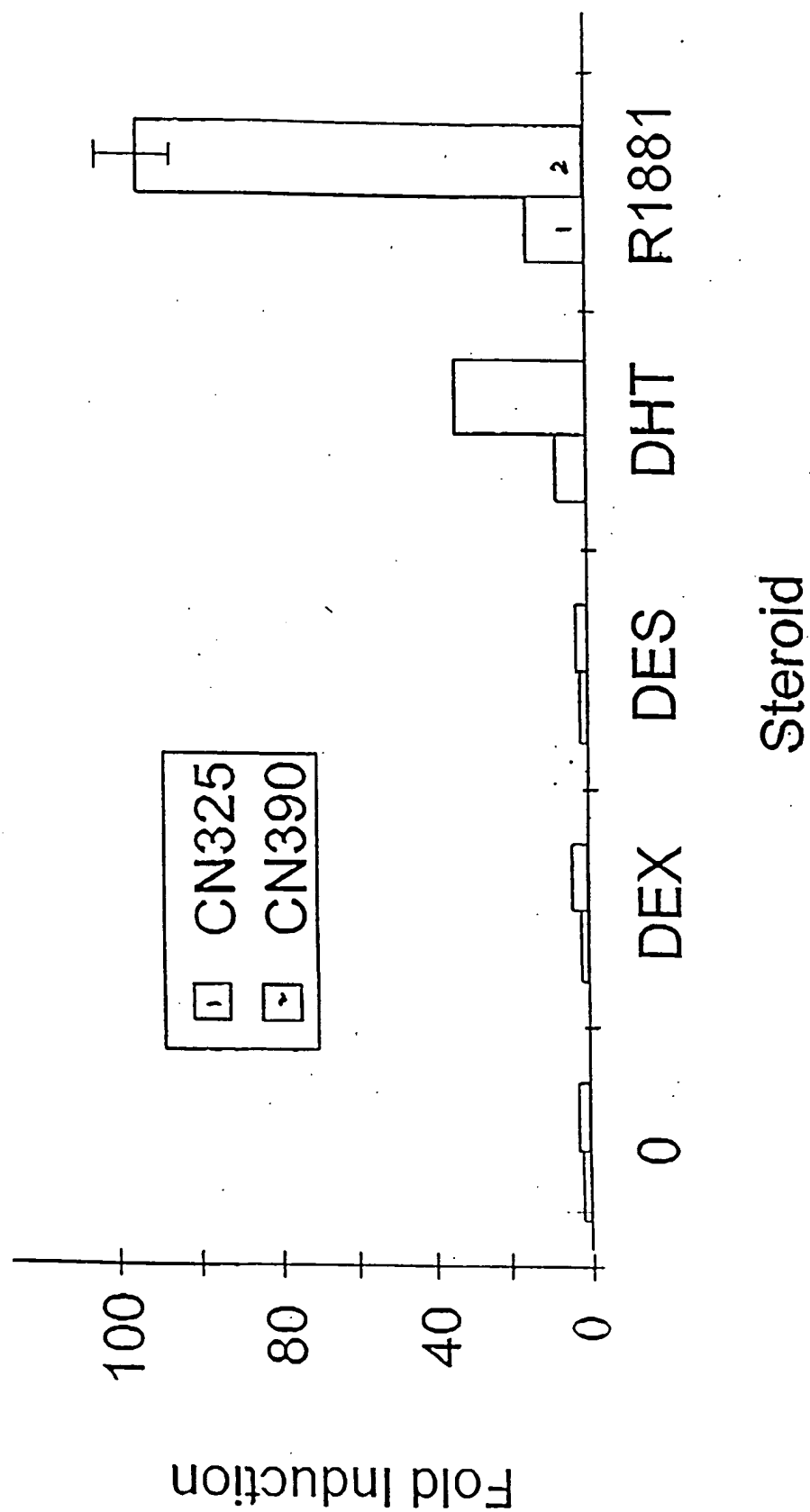
FIGURE 12

**FIGURE 13**

**FIGURE 14**
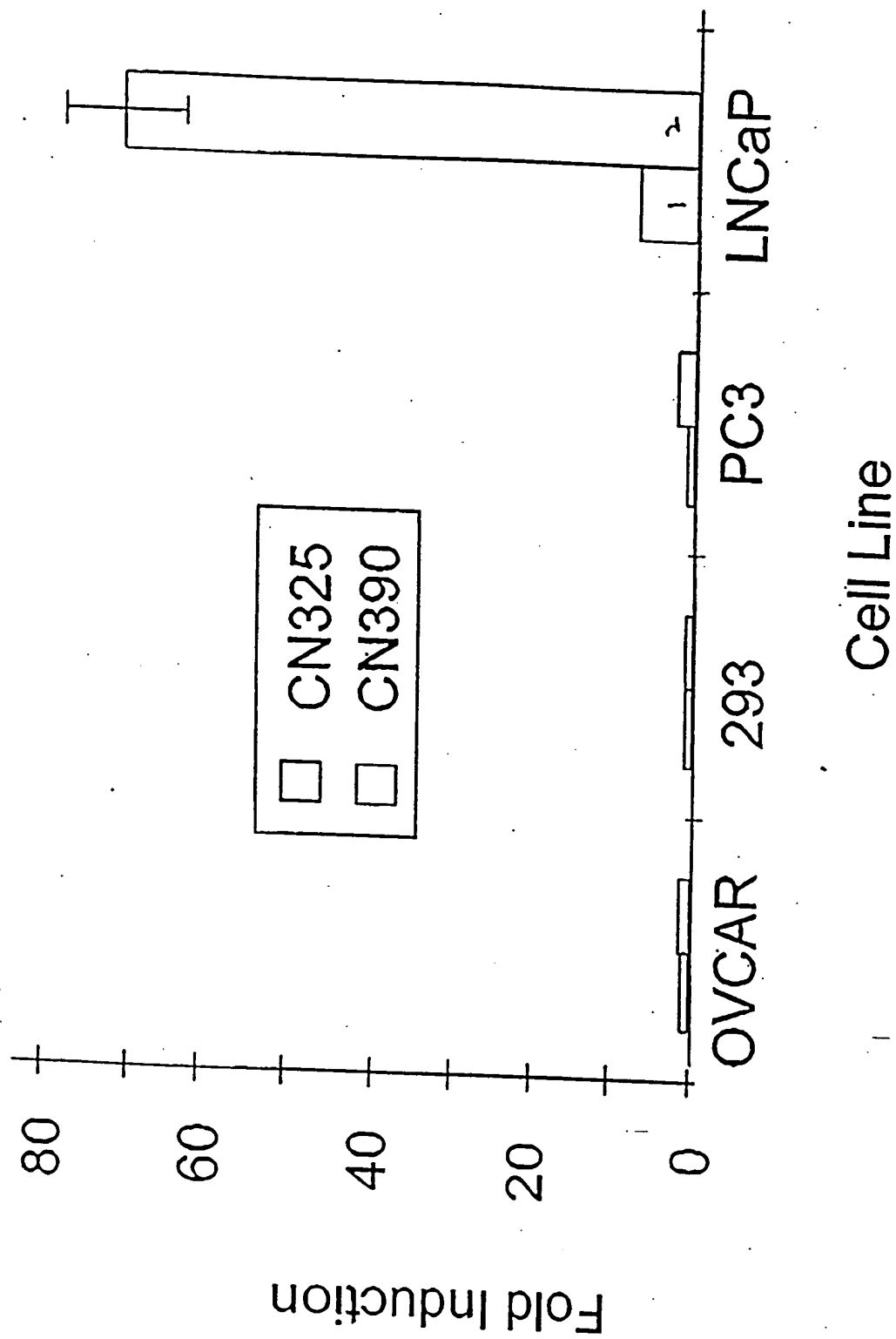
**FIGURE 15**
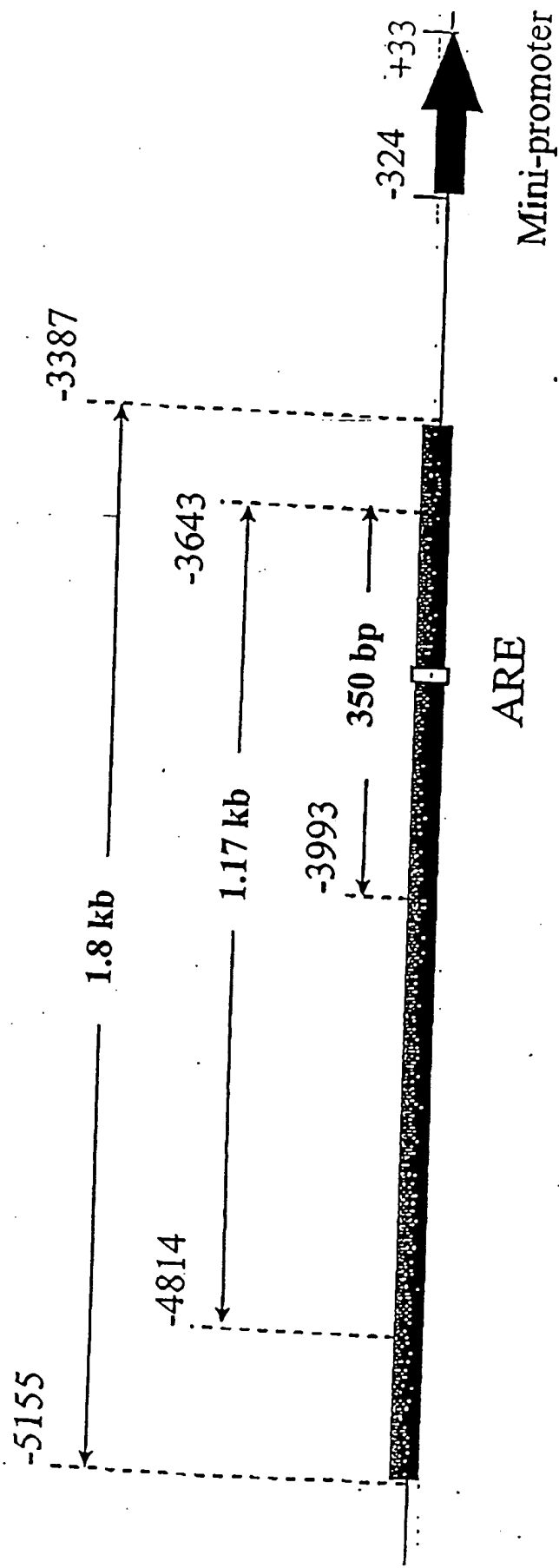
FIGURE 16
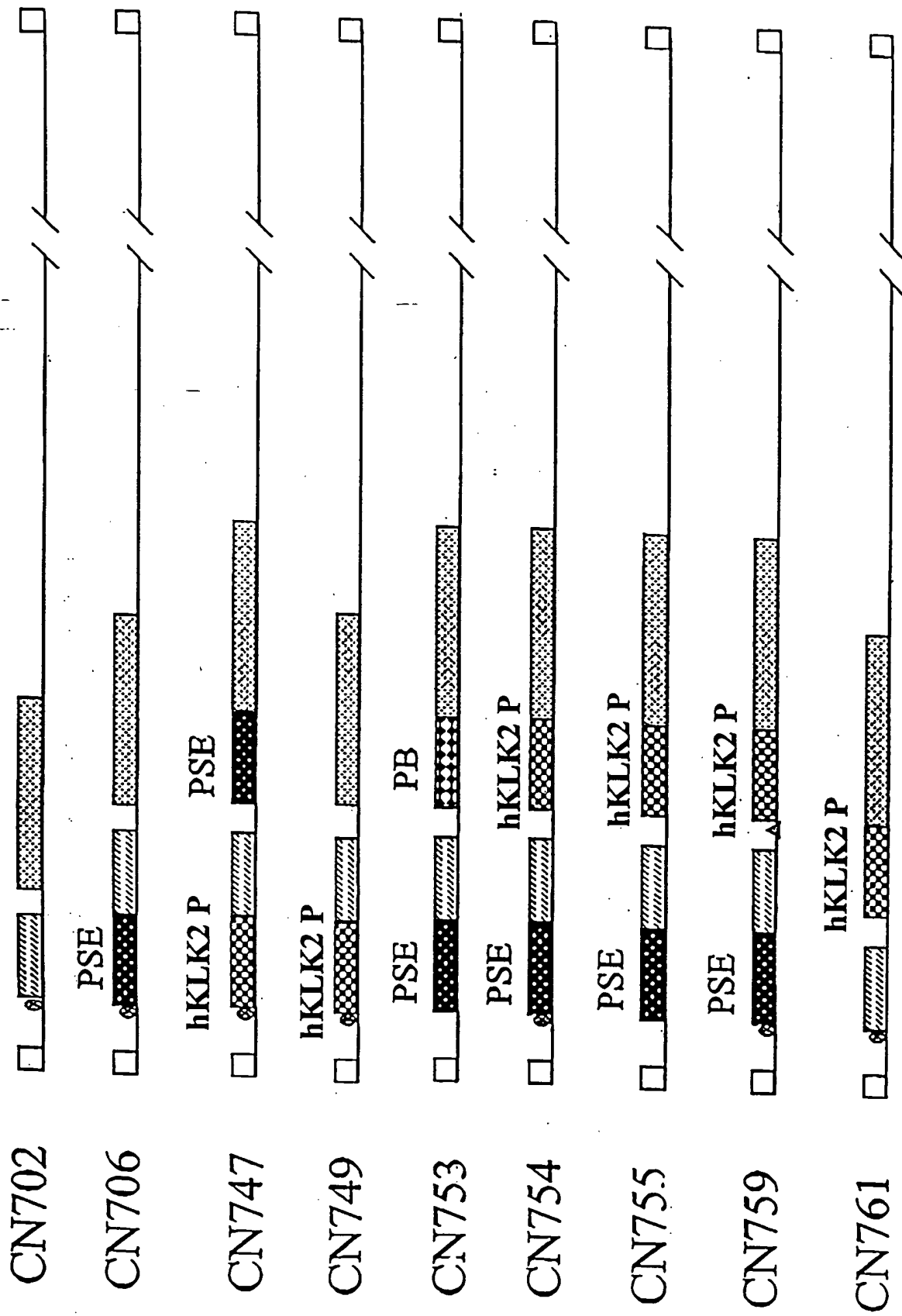
**FIGURE 17A**
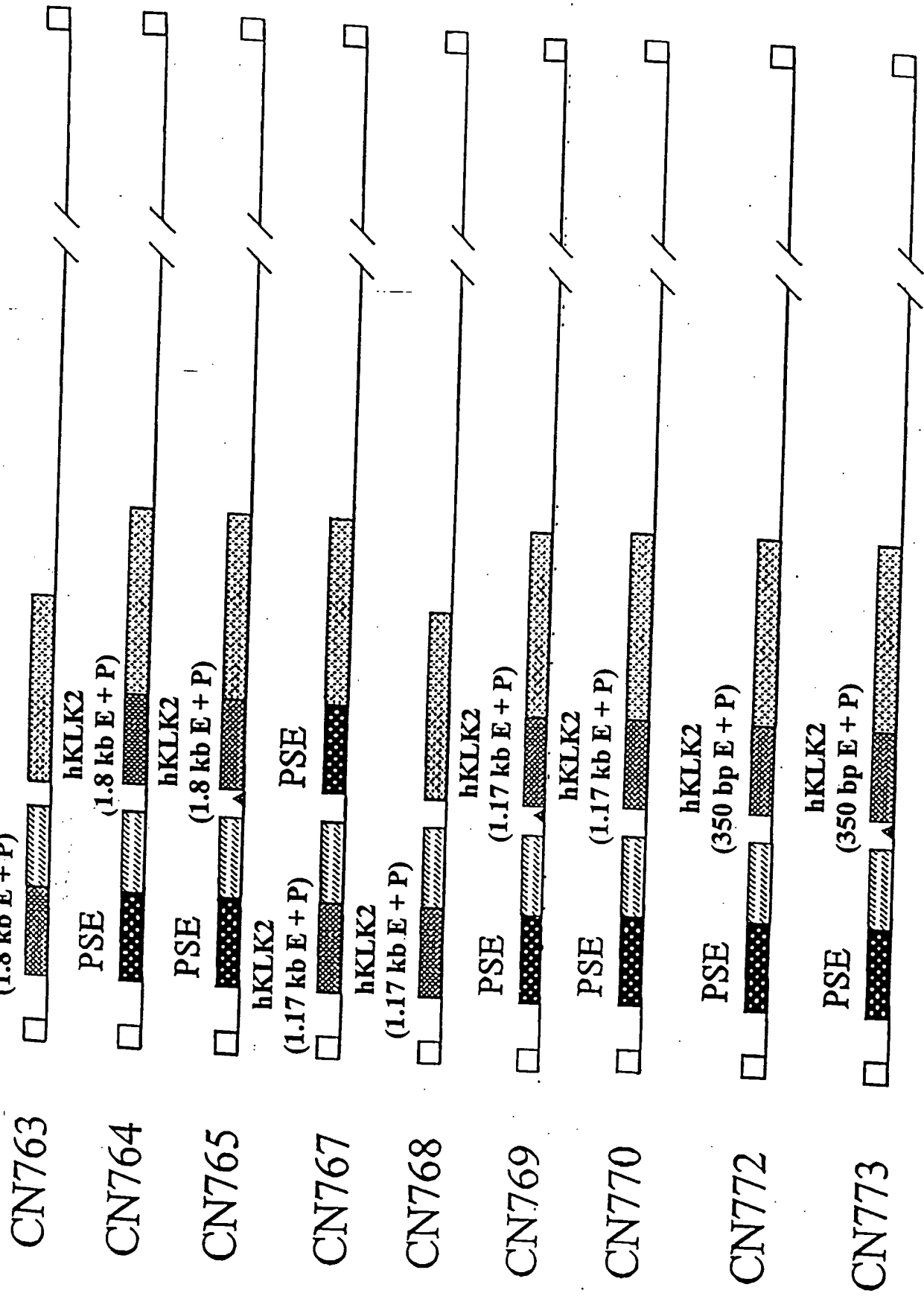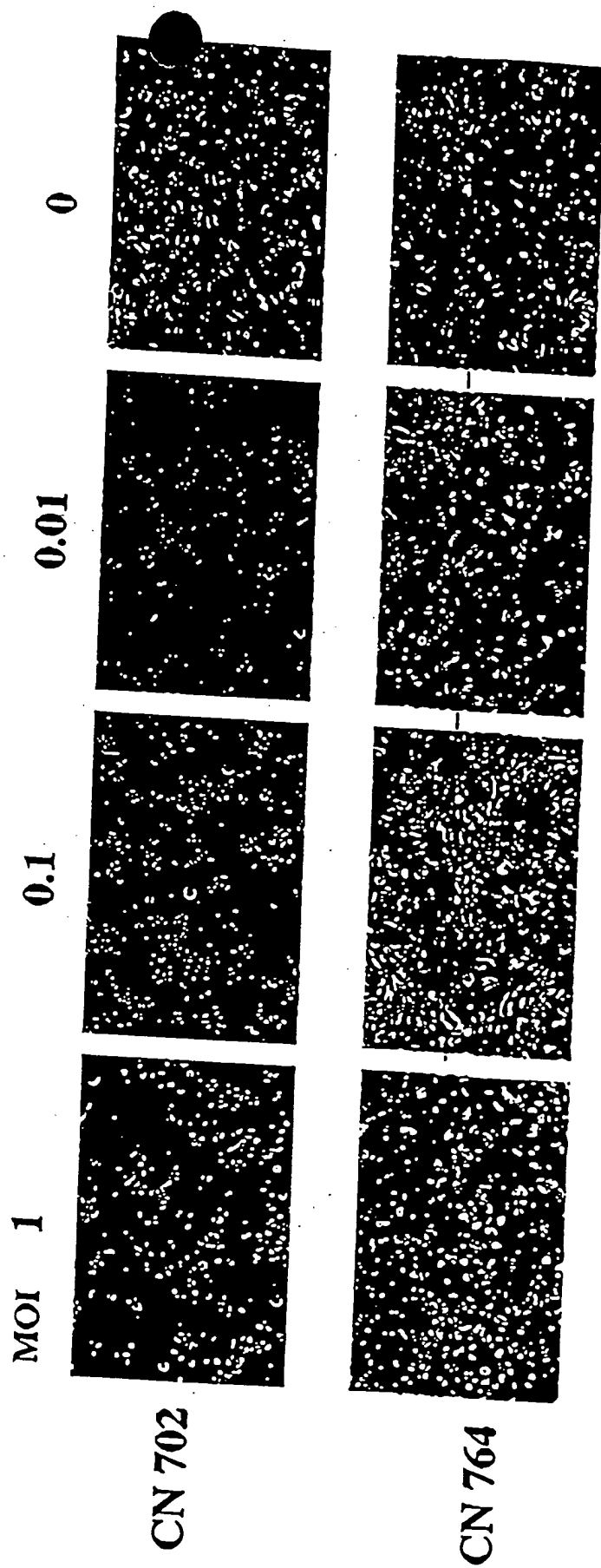
**FIGURE 17B**

FIGURE 18
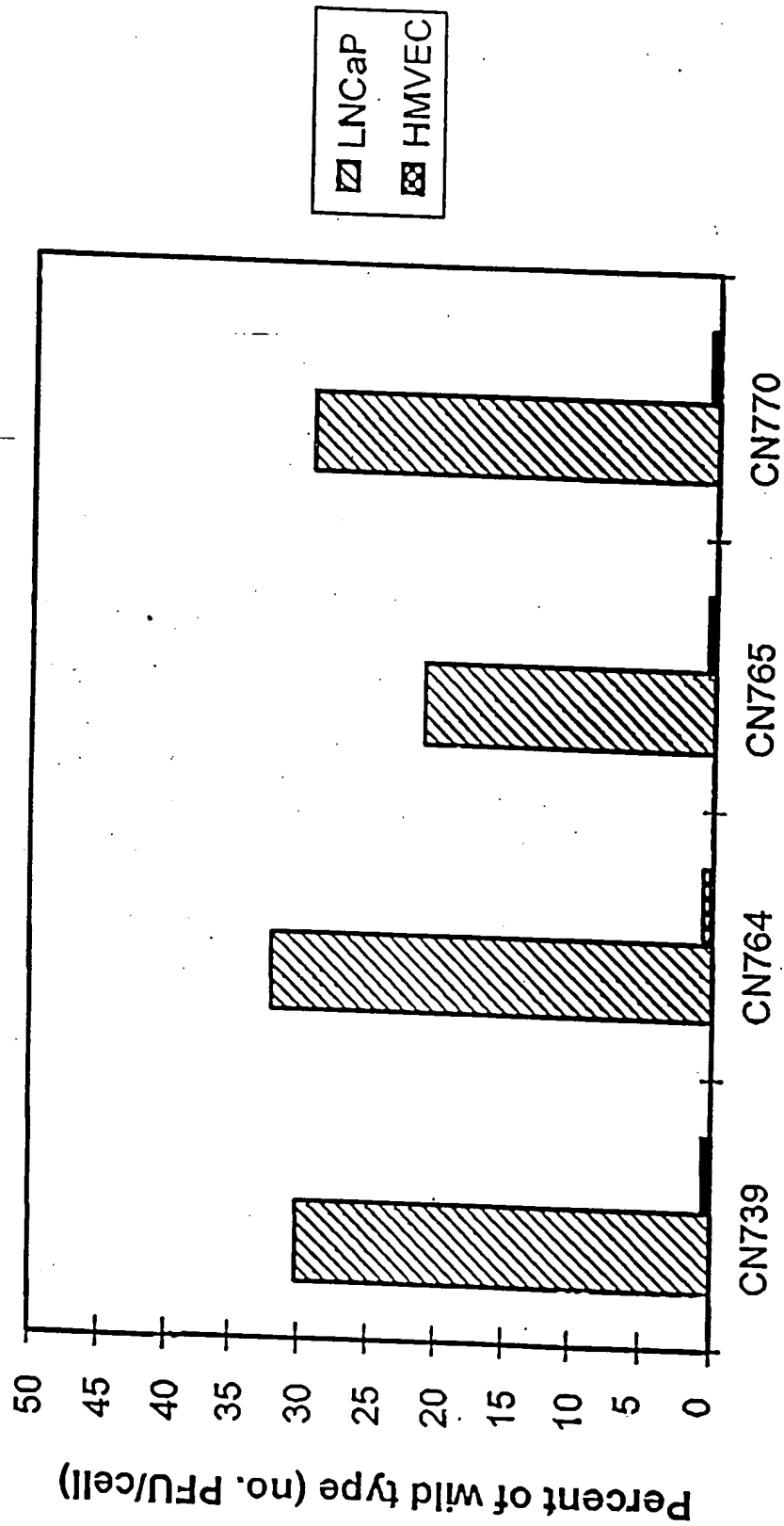
**FIGURE 19**
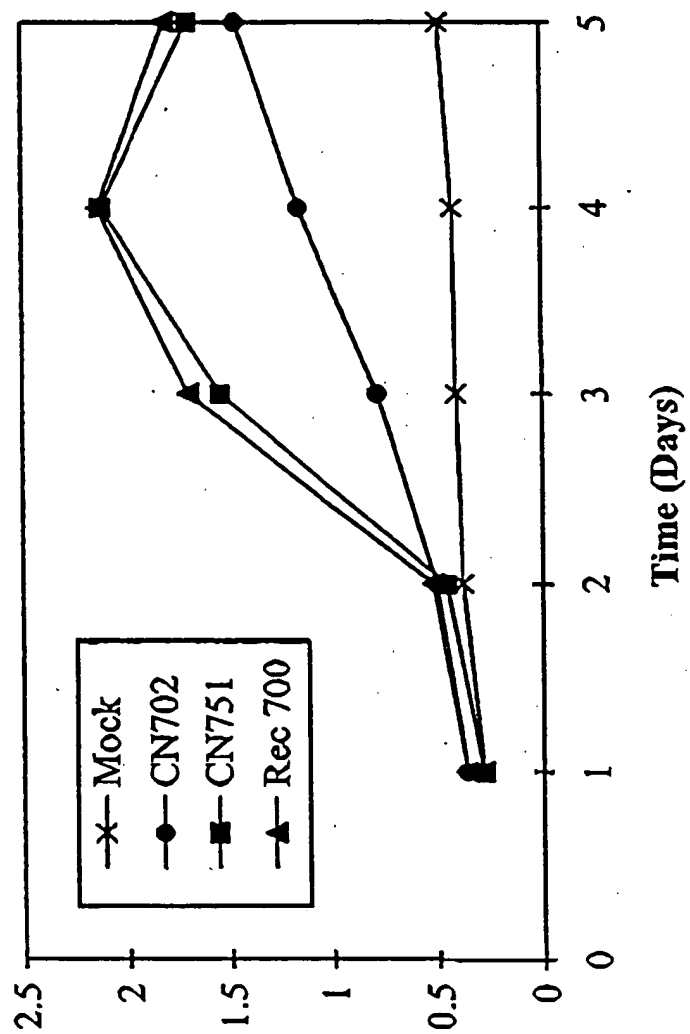
**FIGURE 20**
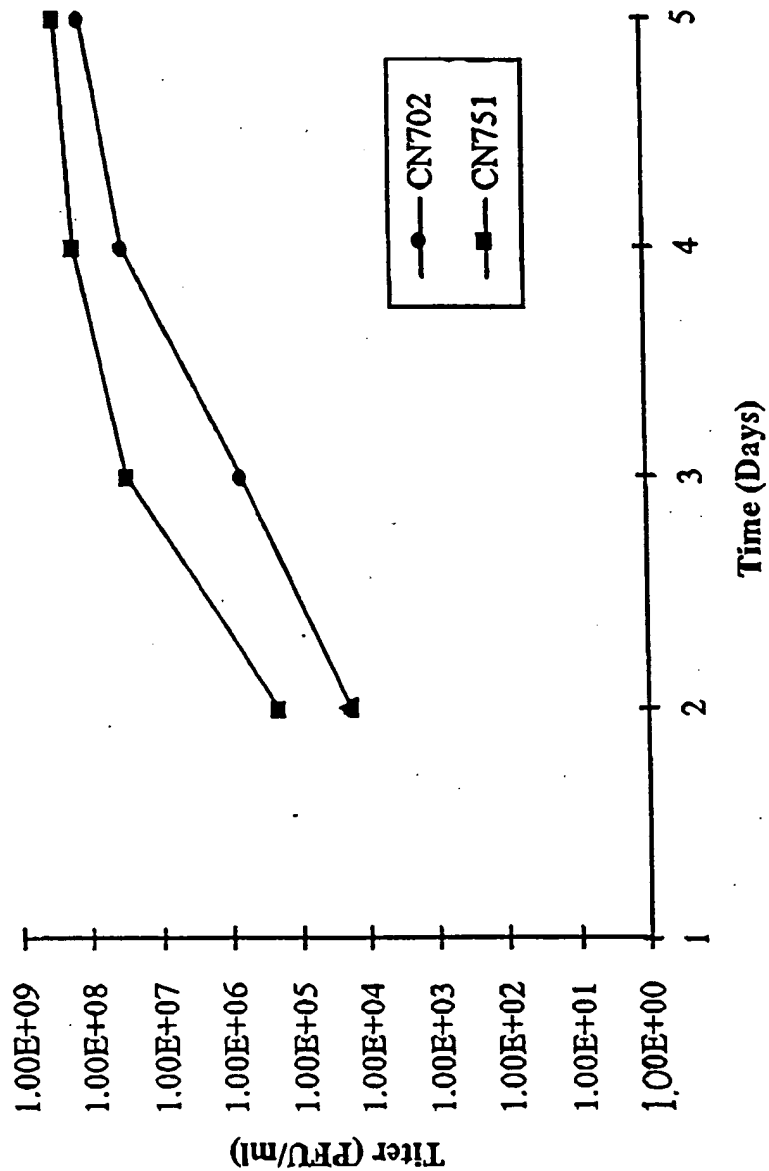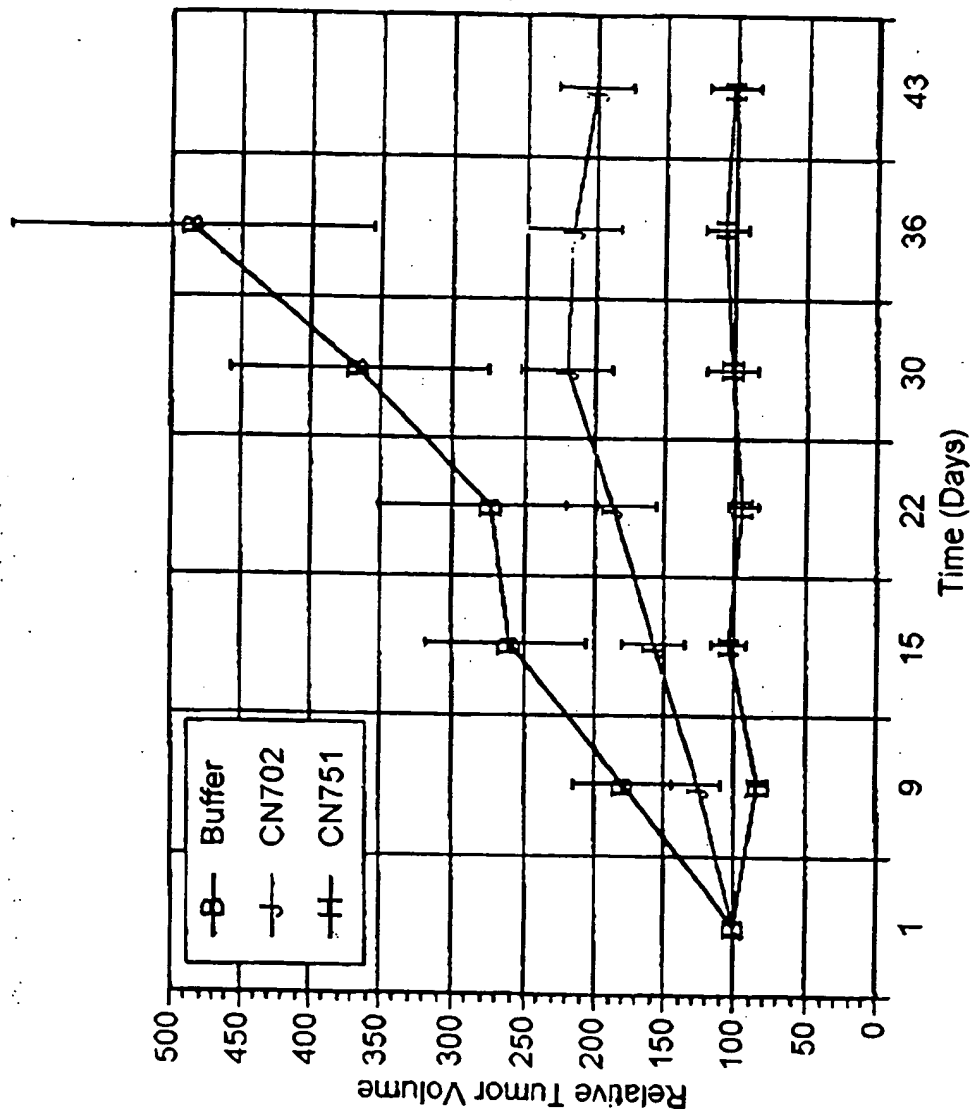
FIGURE 21

**FIGURE 22**

**FIGURE 23A**

Cells

1
Seed Cells

hKLK2-TRE - REPORTER GENE
in Adenovirus

2

Infect
Incubate 1-5 hrs
Add Agent

96 well microtiter plate

Incubate 12-24 hrs

3
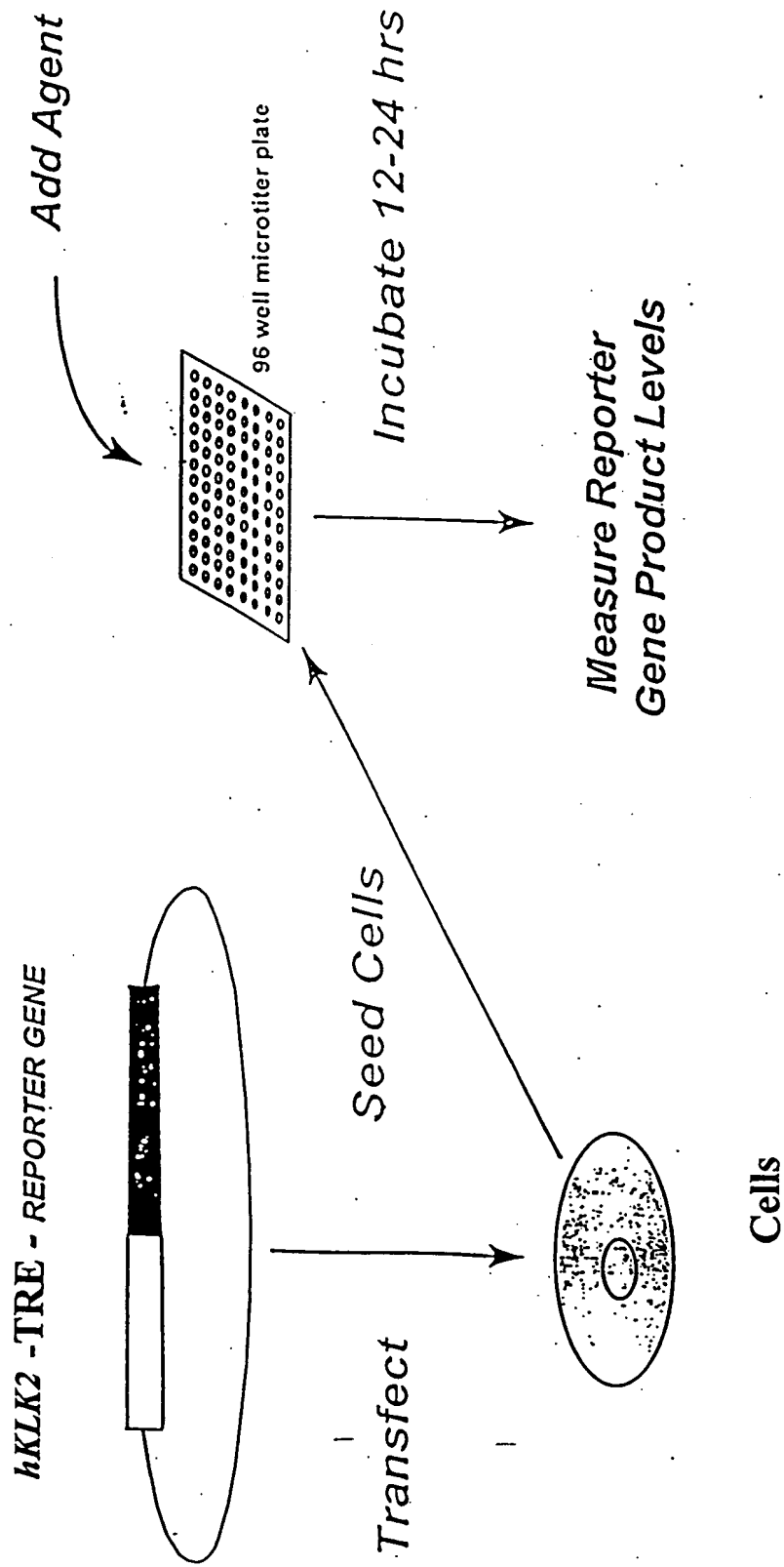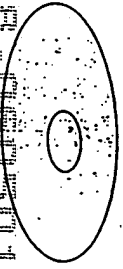
Measure Reporter
Gene Product Levels
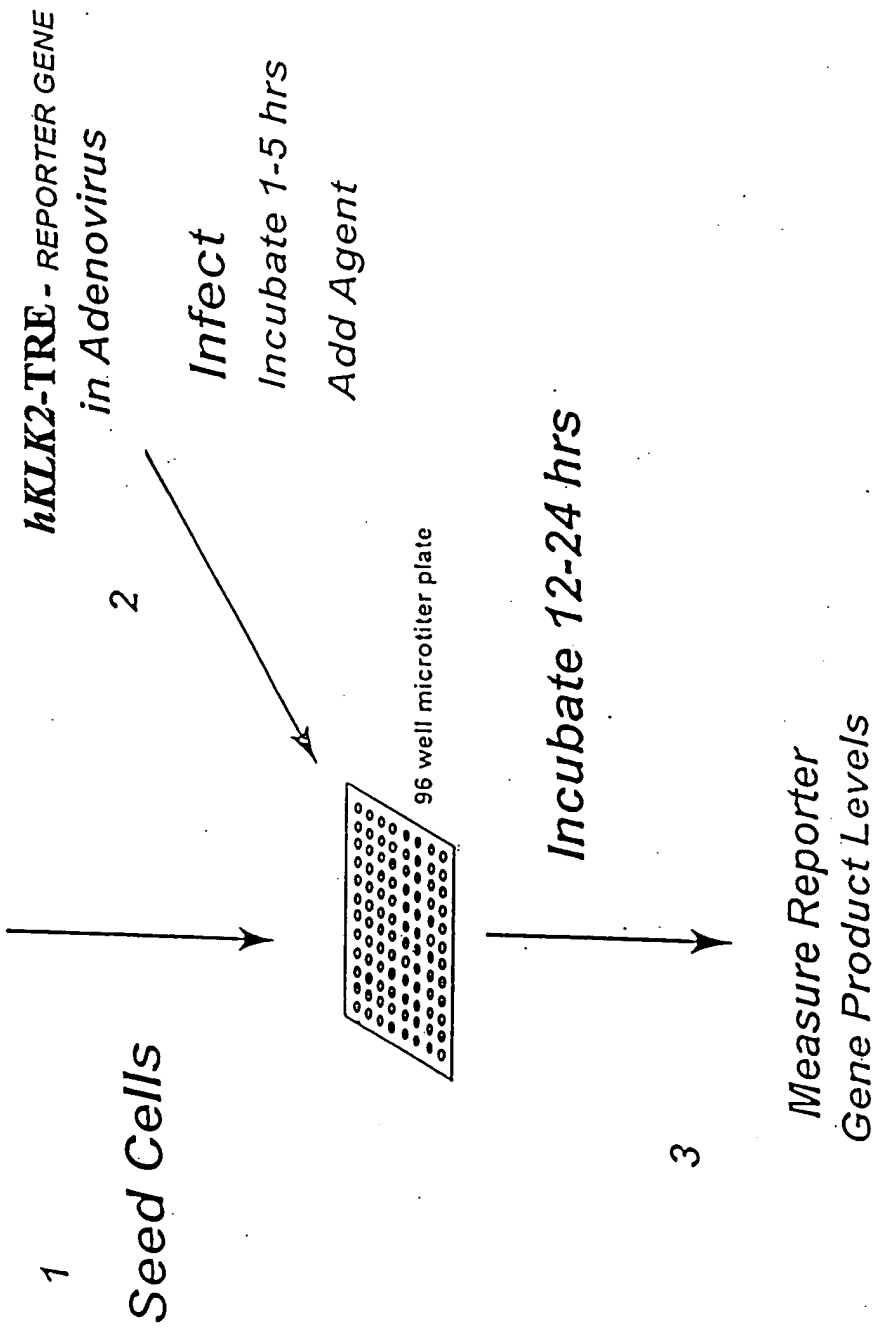
FIGURE 23B

FIGURE 24A

**FIGURE 24B**

| Lane | 1 | 2 | 3 | 4 | 5 | 6 |
|------|---|---|---|---|---|---|
| Protein | - | LN | LN | LN | LN | - |
| Probe | W T | W T | W T | W T | W T | Neg | Neg |
| Competitor | - | - | W T | Neg | - | - |
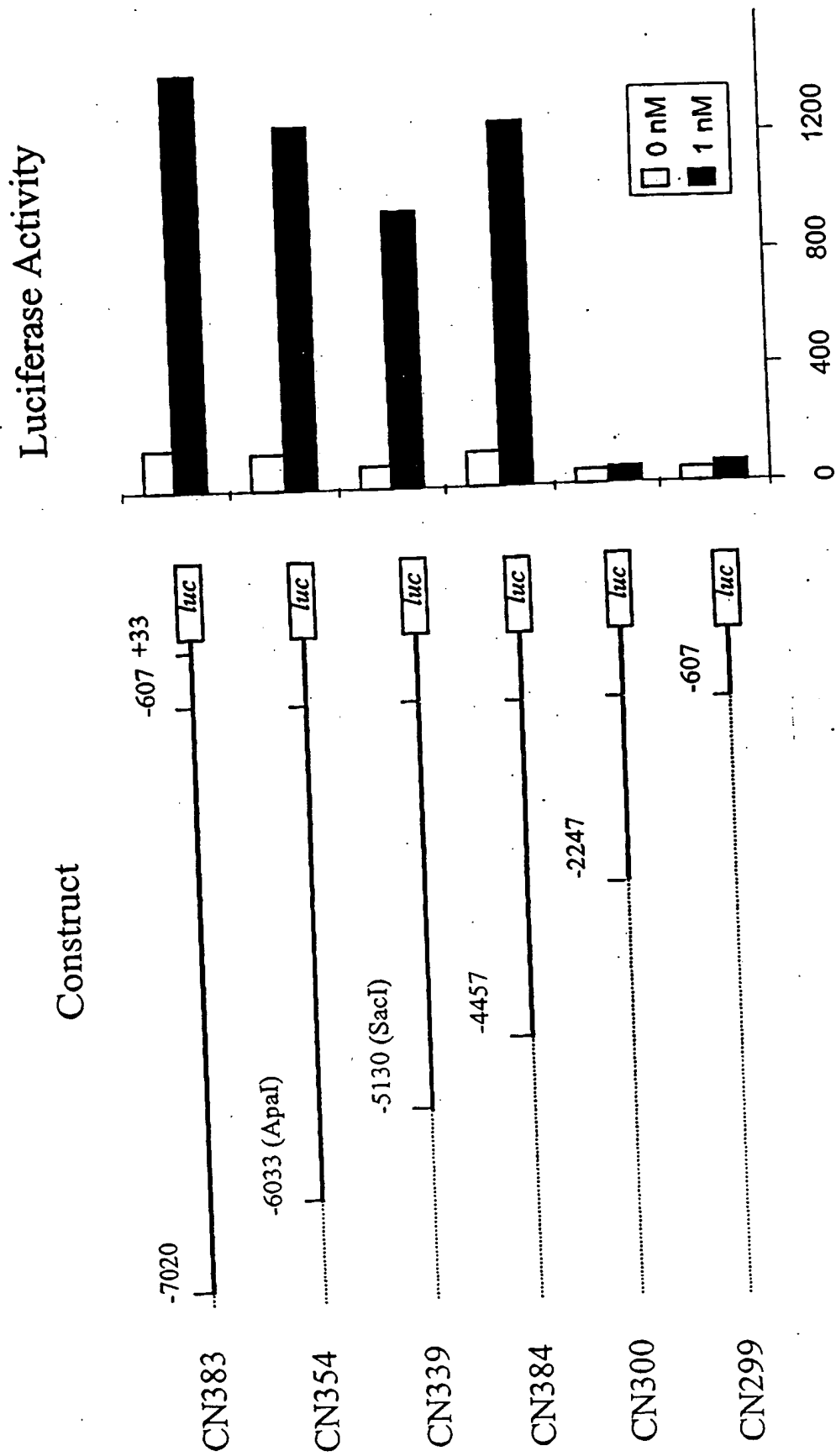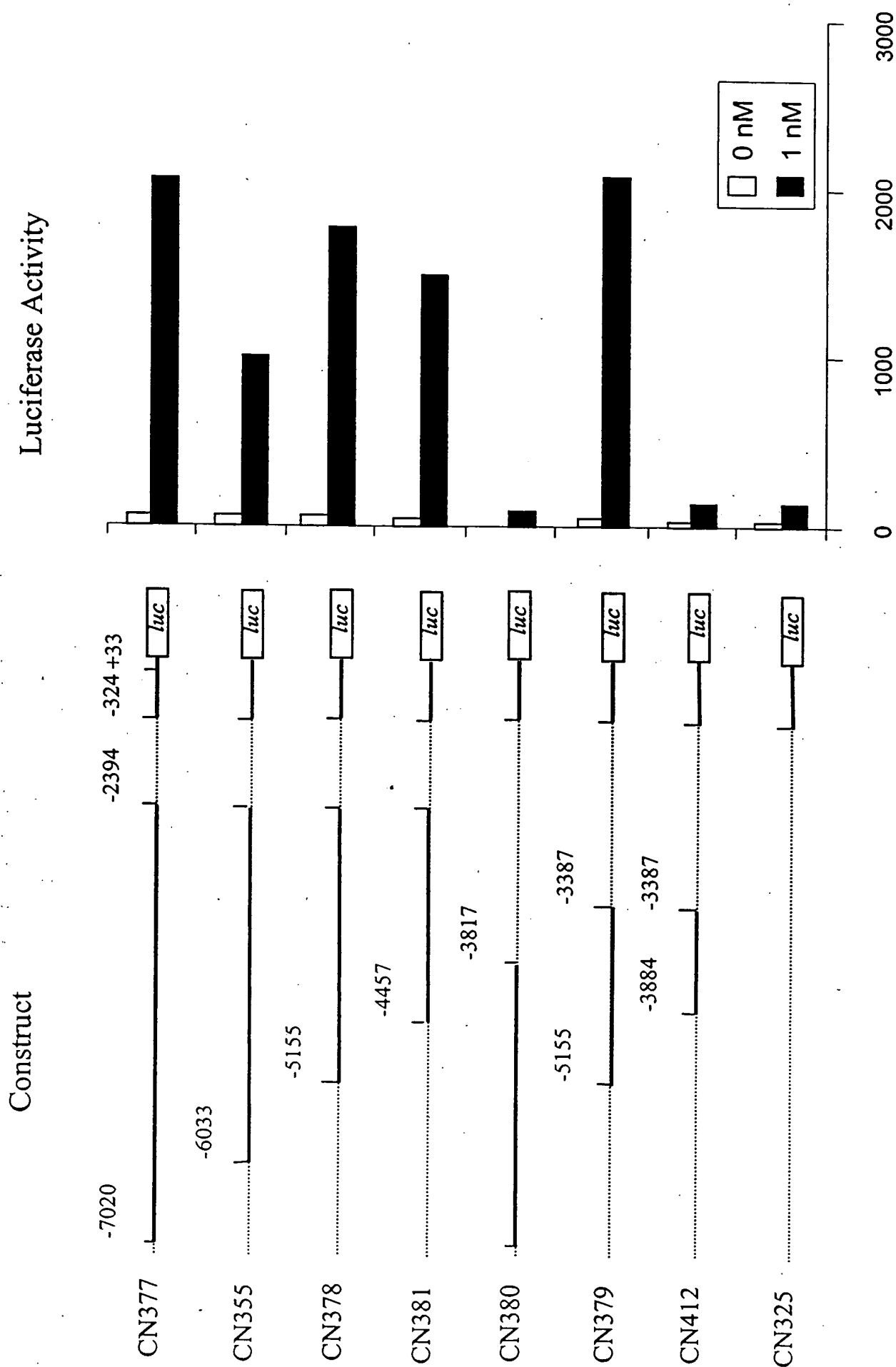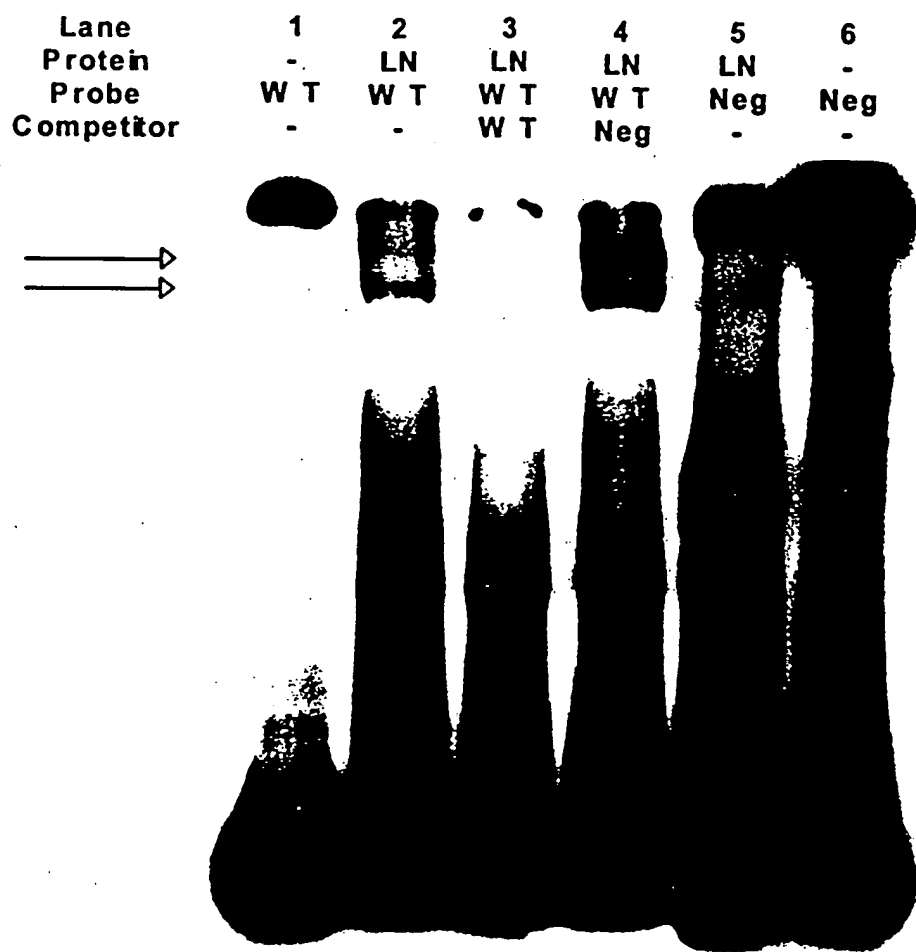
**FIGURE 25A**

| Lane | 1 | 2 | 3 | 4 | 5 |
|------|---|---|---|---|---|
| Protein | - | LN | LN | He | He |
| Competitor | - | - | + | - | + |

## FIGURE 25B

**FIGURE 26**